



48

SEQUENCE LISTING

<110> Creech, Christopher D.  
Jegla, Timothy J.  
ICAgen, Inc.

<120> CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel

<130> 018512-006010US

<140> US 09/855,828

<141> 2001-05-14

<150> US 60/204,445

<151> 2000-05-15

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 809

<212> PRT

<213> Homo sapiens

<220>

<223> human cyclic nucleotide-gated cation channel (CNG)  
3B (CNG3B)

<400> 1

Met Phe Lys Ser Leu Thr Lys Val Asn Lys Val Lys Pro Ile Gly Glu  
1 5 10 15

Asn Asn Glu Asn Glu Gln Ser Ser Arg Arg Asn Glu Glu Gly Ser His  
20 25 30

Pro Ser Asn Gln Ser Gln Gln Thr Thr Ala Gln Glu Glu Asn Lys Gly  
35 40 45

Glu Glu Lys Ser Leu Lys Thr Lys Ser Thr Pro Val Thr Ser Glu Glu  
50 55 60

Pro His Thr Asn Ile Gln Asp Lys Leu Ser Lys Lys Asn Ser Ser Gly  
65 70 75 80

Asp Leu Thr Thr Asn Pro Asp Pro Gln Asn Ala Ala Glu Pro Thr Gly  
85 90 95

Thr Val Pro Glu Gln Lys Glu Met Asp Pro Gly Lys Glu Gly Pro Asn  
100 105 110

Ser Pro Gln Asn Lys Pro Pro Ala Ala Pro Val Ile Asn Glu Tyr Ala  
115 120 125

Asp Ala Gln Leu His Asn Leu Val Lys Arg Met Arg Gln Arg Thr Ala  
130 135 140

Leu Tyr Lys Lys Lys Leu Val Glu Gly Asp Leu Ser Ser Pro Glu Ala  
145 150 155 160

Ser Pro Gln Thr Ala Lys Pro Thr Ala Val Pro Pro Val Lys Glu Ser  
 165 170 175  
 Asp Asp Lys Pro Thr Glu His Tyr Tyr Arg Leu Leu Trp Phe Lys Val  
 180 185 190  
 Lys Lys Met Pro Leu Thr Glu Tyr Leu Lys Arg Ile Lys Leu Pro Asn  
 195 200 205  
 Ser Ile Asp Ser Tyr Thr Asp Arg Leu Tyr Leu Leu Trp Leu Leu Leu  
 210 215 220  
 Val Thr Leu Ala Tyr Asn Trp Asn Cys Trp Phe Ile Pro Leu Arg Leu  
 225 230 235 240  
 Val Phe Pro Tyr Gln Thr Ala Asp Asn Ile His Tyr Trp Leu Ile Ala  
 245 250 255  
 Asp Ile Ile Cys Asp Ile Ile Tyr Leu Tyr Asp Met Leu Phe Ile Gln  
 260 265 270  
 Pro Arg Leu Gln Phe Val Arg Gly Gly Asp Ile Ile Val Asp Ser Asn  
 275 280 285  
 Glu Leu Arg Lys His Tyr Arg Thr Ser Thr Lys Phe Gln Leu Asp Val  
 290 295 300  
 Ala Ser Ile Ile Pro Phe Asp Ile Cys Tyr Leu Phe Phe Gly Phe Asn  
 305 310 315 320  
 Pro Met Phe Arg Ala Asn Arg Met Leu Lys Tyr Thr Ser Phe Phe Glu  
 325 330 335  
 Phe Asn His His Leu Glu Ser Ile Met Asp Lys Ala Tyr Ile Tyr Arg  
 340 345 350  
 Val Ile Arg Thr Thr Gly Tyr Leu Leu Phe Ile Leu His Ile Asn Ala  
 355 360 365  
 Cys Val Tyr Tyr Trp Ala Ser Asn Tyr Glu Gly Ile Gly Thr Thr Arg  
 370 375 380  
 Trp Val Tyr Asp Gly Glu Gly Asn Glu Tyr Leu Arg Cys Tyr Tyr Trp  
 385 390 395 400  
 Ala Val Arg Thr Leu Ile Thr Ile Gly Gly Leu Pro Glu Pro Gln Thr  
 405 410 415  
 Leu Phe Glu Ile Val Phe Gln Leu Leu Asn Phe Phe Ser Gly Val Phe  
 420 425 430  
 Val Phe Ser Ser Leu Ile Gly Gln Met Arg Asp Val Ile Gly Ala Ala  
 435 440 445  
 Thr Ala Asn Gln Asn Tyr Phe Arg Ala Cys Met Asp Asp Thr Ile Ala  
 450 455 460  
 Tyr Met Asn Asn Tyr Ser Ile Pro Lys Leu Val Gln Lys Arg Val Arg  
 465 470 475 480

Thr	Trp	Tyr	Glu	Tyr	Thr	Trp	Asp	Ser	Gln	Arg	Met	Leu	Asp	Glu	Ser	485	490	495
Asp	Leu	Leu	Lys	Thr	Leu	Pro	Thr	Thr	Val	Gln	Leu	Ala	Leu	Ala	Ile	500	505	510
Asp	Val	Asn	Phe	Ser	Ile	Ile	Ser	Lys	Val	Asp	Leu	Phe	Lys	Gly	Cys	515	520	525
Asp	Thr	Gln	Met	Ile	Tyr	Asp	Met	Leu	Leu	Arg	Leu	Lys	Ser	Val	Leu	530	535	540
Tyr	Leu	Pro	Gly	Asp	Phe	Val	Cys	Lys	Lys	Gly	Glu	Ile	Gly	Lys	Glu	545	550	555
Met	Tyr	Ile	Ile	Lys	His	Gly	Glu	Val	Gln	Val	Leu	Gly	Gly	Pro	Asp	565	570	575
Gly	Thr	Lys	Val	Leu	Val	Thr	Leu	Lys	Ala	Gly	Ser	Val	Phe	Gly	Glu	580	585	590
Ile	Ser	Leu	Leu	Ala	Ala	Gly	Gly	Gly	Asn	Arg	Arg	Thr	Ala	Asn	Val	595	600	605
Val	Ala	His	Gly	Phe	Ala	Asn	Leu	Leu	Thr	Leu	Asp	Lys	Lys	Thr	Leu	610	615	620
Gln	Glu	Ile	Leu	Val	His	Tyr	Pro	Asp	Ser	Glu	Arg	Ile	Leu	Met	Lys	625	630	635
Lys	Ala	Arg	Val	Leu	Leu	Lys	Gln	Lys	Ala	Lys	Thr	Ala	Glu	Ala	Thr	645	650	655
Pro	Pro	Arg	Lys	Asp	Leu	Ala	Leu	Leu	Phe	Pro	Pro	Lys	Glu	Glu	Thr	660	665	670
Pro	Lys	Leu	Phe	Lys	Thr	Leu	Leu	Gly	Gly	Thr	Gly	Lys	Ala	Ser	Leu	675	680	685
Ala	Arg	Leu	Leu	Lys	Leu	Lys	Arg	Glu	Gln	Ala	Ala	Gln	Lys	Lys	Glu	690	695	700
Asn	Ser	Glu	Gly	Gly	Glu	Glu	Glu	Gly	Lys	Glu	Asn	Glu	Asp	Lys	Gln	705	710	715
Lys	Glu	Asn	Glu	Asp	Lys	Gln	Lys	Glu	Asn	Glu	Asp	Lys	Gly	Lys	Glu	725	730	735
Asn	Glu	Asp	Lys	Asp	Lys	Gly	Arg	Glu	Pro	Glu	Glu	Lys	Pro	Leu	Asp	740	745	750
Arg	Pro	Glu	Cys	Thr	Ala	Ser	Pro	Ile	Ala	Val	Glu	Glu	Glu	Pro	His	755	760	765
Ser	Val	Arg	Arg	Thr	Val	Leu	Pro	Arg	Gly	Thr	Ser	Arg	Gln	Ser	Leu	770	775	780

Ile Ile Ser Met Ala Pro Ser Ala Glu Gly Gly Glu Glu Val Leu Thr  
 785 790 795 800

Ile Glu Val Lys Glu Lys Ala Lys Gln  
 805

<210> 2

<211> 2703

<212> DNA

<213> Homo sapiens

<220>

<223> complete human CNG3B nucleotide sequence

<220>

<221> CDS

<222> (63)..(2492)

<223> CNG3B

<400> 2

```

catttctcta ccttaaggca cagtcataaa tacagaggggt tttcagaacc acctcagaga 60
agatgttttaa atcgctgaca aaagtcaaca aggtgaagcc tataggagag aacaatgaga 120
atgaacaaag ttctcgtcgg aatgaagaag gctctcacc aagtaatcag tctcagcaaa 180
ccacagcaca ggaagaaaac aaaggtgaag agaaatctct caaaaccaag tcaactccag 240
tcacgtctga agagccacac accaacatac aagacaaact ctccaagaaa aattcctctg 300
gagatctgac cacaaaaccct gaccctcaaa atgcagcaga accaactgga acagtgccag 360
agcagaagga aatggacccc gggaaagaag gtccaaacag cccacaaaac aaaccgcctg 420
cagctcctgt tataaatgag tatgccgatg ccagctaca caacctgggtg aaaagaatgc 480
gtcaaagaac agccctctac aagaaaaagt tggtagagg agatctctcc tcaccgaag 540
ccagcccaca aactgcaaag ccacggctg taccaccagt aaaagaaagc gatgataagc 600
caacagaaca ttactacagg ctgttgtggt tcaaagtcaa aaagatgcct ttaacagagt 660
acttaaagcg aattaaactt ccaaacagca tagattcata cacagatcga ctctatctcc 720
tgtggctctt gcttgtcact cttgcctata actggaactg ctgggtttata ccactgcgcc 780
tcgtcttccc atatcaaacc gcagacaaca tacactactg gcttattgag gacatcatat 840
gtgatatcat ctacctttat gatatgctat ttatccagcc cagactccag tttgtaagag 900
gaggagacat aatagtggat tcaaatgagc taaggaaaca ctacaggact tctacaaaat 960
ttcagttgga tgcgcacatc ataataccat ttgatatttg ctacctcttc tttgggttta 1020
atccaatggt tagagcaaat aggatgttaa agtacacttc attttttgaa tttaatcatc 1080
acctagagtc tataatggac aaagcatata tctacagagt tattcgaaca actggatact 1140
tgctgtttat tctgcacatt aatgcctgtg tttattactg ggcttcaaac tatgaaggaa 1200
ttggcactac tagatgggtg tatgatgggg aaggaaacga gtatctgaga tgttattatt 1260
gggcagttcg aactttaatt accattgggtg gccttcagaa accacaaact ttatttgaaa 1320
ttgtttttca actcttgaat tttttttctg gagtttttgt gttctccagt ttaattgggtc 1380
agatgagaga tgtgattgga gcagctacag ccaatcagaa ctacttccgc gcctgcatgg 1440
atgacaccat tgcctacatg aacaattact ccattcctaa acttgtgcaa aagcaggttc 1500
ggacttggtg tgaatataca tgggactctc aaagaatgct agatgagtct gatttgctta 1560
agaccctacc aactacggtc cagttagccc tcgccattga tgtgaacttc agcatcatca 1620
gcaaagtcca cttgttcaag ggttgtgata cacagatgat ttatgacatg ttgctaagat 1680
tgaaatccgt tctctatttg cctggtgact ttgtctgcaa aaaggagaaa attggcaagg 1740
aaatgtatat catcaagcat ggagaagtc aagttcttgg aggccctgat ggtactaaag 1800
ttctggttac tctgaaagct gggtcggtgt ttggagaaat cagccttcta gcagcaggag 1860
gaggaaaccg tcgaactgcc aatgtgggtg ccacgggtt tgccaatctt ttaactctag 1920
acaaaaagac cctccaagaa attctagtgc attatccaga ttctgaaagg atcctcatga 1980
agaaagccag agtgctttta aagcagaagg ctaagaccgc agaagcaacc cctccaagaa 2040
aagatcttgc cctcctcttc ccaccgaaag aagagacacc caaactgttt aaaactctcc 2100
taggaggcag aggaaaagca agtcttgcaa gactactcaa attgaagcga gagcaagcag 2160
ctcagaagaa agaaaattct gaaggaggag aggaagaagg aaaagaaaaat gaagataaac 2220
aaaaagaaaa tgaagataaa caaaaagaaa atgaagataa aggaaaagaa aatgaagata 2280
aagataaagg aagagagcca gaagagaagc cactggacag acctgaatgt acagcaagtc 2340
ctattgcagt ggaggaagaa cccactcag ttagaaggac agttttacc agagggactt 2400

```

```

ctcgtcaatc actcattatc agcatggctc cttctgctga gggcggagaa gaggtttctta 2460
ctattgaagt caaagaaaag gctaagcaat aaatgtttga ttatcttttag atgtgatata 2520
gctagttccc aaagtgattg tacctaggat tgtaacttaa attaacgagg ggaacgaca 2580
tgctgggacc cttgagaaac gaaaggcaaa tccctagctt agtttctagg acttatctga 2640
gagtgtgatt tcatgcagtg gtaataagaa gattattaaa agcaaaaaaa aaaaaaaaaa 2700
aaa                                              2703

```

```

<210> 3
<211> 2430
<212> DNA
<213> Homo sapiens

```

```

<220>
<223> human CNG3B coding sequence

```

```

<220>
<221> CDS
<222> (1) .. (2430)
<223> CNG3B

```

```

<400> 3
atgtttaaat cgctgacaaa agtcaacaag gtgaagccta taggagagaa caatgagaat 60
gaacaaagtt ctcgtcggaa tgaagaaggc tctcacccaa gtaatcagtc tcagcaaacc 120
acagcacagg aagaaaacaa aggtgaagag aaatctctca aaaccaagtc aactccagtc 180
acgtctgaag agccacacac caacatacaa gacaaactct ccaagaaaaa ttctcttgga 240
gatctgacca caaacctga ccctcaaaat gcagcagaac caactggaac agtgccagag 300
cagaaggaaa tggaccccg gaaagaaggc ccaaacagcc cacaaaacaa accgcctgca 360
gctcctgtta taaatgagta tgccgatgcc cagctacaca acctggtgaa aagaatgcgt 420
caaagaacag ccctctacaa gaaaaagttg gtgaggggag atctctcctc accgaagcc 480
agcccacaaa ctgcaaagcc cacggctgta ccaccagtaa aagaaagcga tgataagcca 540
acagaacatt actacaggct gttgtggttc aaagtcaaaa agatgccttt aacagagtac 600
ttaaagcgaa ttaaacttcc aaacagcata gattcataca cagatcgact ctatctcctg 660
tggtccttgc ttgtcactct tgcctataac tggaaactgct ggtttatacc actgcgcctc 720
gtcttcccat atcaaaccgc agacaacata cactactggc ttattgcgga catcatatgt 780
gatatcatct acctttatga tatgtatatt atccagccca gactccagtt tgtaagagga 840
ggagacataa tagtggattc aaatgagcta aggaaacact acaggacttc taaaaattt 900
cagttggatg tcgcatcaat aataccattt gatatttgct acctcttctt tgggtttaat 960
ccaatgttta gagcaaatag gatgttaaa gacacttcat tttttgaatt taatcatcac 1020
ctagagtcta taatggacaa agcatatatc tacagagtta ttcgaacaac tggatacttg 1080
ctgtttattc tgcacattaa tgctgtgtt tattactggg cttcaaacta tgaagggaatt 1140
ggcactacta gatgggtgta tgatggggaa ggaaacgagt atctgagatg ttattatttg 1200
gcagttcgaa cttaattac cattggtggc cttccagaac caaaaacttt atttgaaatt 1260
gtttttcaac tcttgaattt tttttctgga gtttttgtgt tctccagttt aattggtcag 1320
atgagagatg tgattggagc agctacagcc aatcagaact acttccgcgc ctgcatggat 1380
gacaccattg cctacatgaa caattactcc attcctaaac ttgtgcaaaa gcgagttcgg 1440
acttggtatg aatatacatg ggactctcaa agaattgctag atgagtctga tttgcttaag 1500
accctaccaa ctacgggtcca gttagccctc gccattgatg tgaacttcag catcatcagc 1560
aaagtcgact tgttcaaggg ttgtgataca ccagatgattt atgacatgtt gctaagattg 1620
aaatccgttc tctatttgcc tggtagcttt gtctgcaaaa agggagaaat tggcaaggaa 1680
atgtatatca tcaagcatgg agaagtccaa gttcttgagg gccctgatgg tactaaagtt 1740
ctggttactc tgaaagctgg gtcggtgttt ggagaaatca gccttctagc agcaggagga 1800
ggaaaccgtc gaactgccaa tgtggtggcc cacgggtttg ccaatctttt aactctagac 1860
aaaaagaccc tccaagaaat tctagtgcac tatccagatt ctgaaaggat cctcatgaag 1920
aaagccagag tgctttttaa gcagaaggct aagaccgcag aagcaacccc tccaagaaaa 1980
gatcttgccc tctcttccc accgaaagaa gagacacca aactgtttaa aactctccta 2040
ggaggcacag gaaaagcaag tcttgcaaga tactcaaat tgaagcgaga gcaagcagct 2100
cagaagaaag aaaattctga aggaggagag gaagaaggaa aagaaaatga agataaaca 2160
aaagaaaatg aagataaaca aaaagaaaat gaagataaag gaaaagaaaa tgaagataaa 2220
gataaaggaa gagagccaga agagaagcca ctggacagac ctgaatgtac agcaagtcct 2280
attgcagtgg aggaagaacc ccactcagtt agaaggacag ttttaccagc agggacttct 2340

```

cgtcaatcac tcattatcag catggctcct tctgctgagg gcggagaaga ggttcttact 2400  
attgaagtca aagaaaaggc taagcaataa 2430

<210> 4  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligo 1 5'-(1)  
sense strand primer

<400> 4  
tctatctcct gtggctcttg cttgtc 26

<210> 5  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligo 2 5'-(2)  
antisense strand primer

<400> 5  
gagtctgggc tggataaata gcatatc 27

<210> 6  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligo 3 5'-(3)  
sense strand primer

<400> 6  
aggaattggc actactagat ggggtg 25

<210> 7  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligo 4 5'-(4)  
antisense strand primer

<400> 7  
ttcatgagga tcctttcaga atctgg 26

<210> 8  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Oligo 5 5'-(5)  
       sense strand primer  
  
 <400> 8  
 ggaaaccgtc gaactgccaa tgtggt 26  
  
 <210> 9  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:Oligo 6 5'-(6)  
       sense strand primer  
  
 <400> 9  
 cgggtttgcc aatcttttaa ctctagac 28  
  
 <210> 10  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:Oligo 7 5'-(7)  
       antisense strand primer  
  
 <400> 10  
 gtccgcaata agccagtagt gtagt 25  
  
 <210> 11  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:Oligo 8 5'-(8)  
       sense strand primer  
  
 <400> 11  
 tgacaagctt ccgcatgtt taaatcgctg acaaaagtc 39  
  
 <210> 12  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:Oligo 9 5'-(9)  
       antisense strand primer  
  
 <400> 12  
 tgacgaattc tcccagcatg tcgtttcccc tcgttaa 37

<210> 13  
 <211> 809  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CNG3B

<400> 13

Met	Phe	Lys	Ser	Leu	Thr	Lys	Val	Asn	Lys	Val	Lys	Pro	Ile	Gly	Glu	1	5	10	15
Asn	Asn	Glu	Asn	Glu	Gln	Ser	Ser	Arg	Arg	Asn	Glu	Glu	Gly	Ser	His	20	25	30	
Pro	Ser	Asn	Gln	Ser	Gln	Gln	Thr	Thr	Ala	Gln	Glu	Glu	Asn	Lys	Gly	35	40	45	
Glu	Glu	Lys	Ser	Leu	Lys	Thr	Lys	Ser	Thr	Pro	Val	Thr	Ser	Glu	Glu	50	55	60	
Pro	His	Thr	Asn	Ile	Gln	Asp	Lys	Leu	Ser	Lys	Lys	Asn	Ser	Ser	Gly	65	70	75	
Asp	Leu	Thr	Thr	Asn	Pro	Asp	Pro	Gln	Asn	Ala	Ala	Glu	Pro	Thr	Gly	85	90	95	
Thr	Val	Pro	Glu	Gln	Lys	Glu	Met	Asp	Pro	Gly	Lys	Glu	Gly	Pro	Asn	100	105	110	
Ser	Pro	Gln	Asn	Lys	Pro	Pro	Ala	Ala	Pro	Val	Ile	Asn	Glu	Tyr	Ala	115	120	125	
Asp	Ala	Gln	Leu	His	Asn	Leu	Val	Lys	Arg	Met	Arg	Gln	Arg	Thr	Ala	130	135	140	
Leu	Tyr	Lys	Lys	Lys	Leu	Val	Glu	Gly	Asp	Leu	Ser	Ser	Pro	Glu	Ala	145	150	155	
Ser	Pro	Gln	Thr	Ala	Lys	Pro	Thr	Ala	Val	Pro	Pro	Val	Lys	Glu	Ser	165	170	175	
Asp	Asp	Lys	Pro	Thr	Glu	His	Tyr	Tyr	Arg	Leu	Leu	Trp	Phe	Lys	Val	180	185	190	
Lys	Lys	Met	Pro	Leu	Thr	Glu	Tyr	Leu	Lys	Arg	Ile	Lys	Leu	Pro	Asn	195	200	205	
Ser	Ile	Asp	Ser	Tyr	Thr	Asp	Arg	Leu	Tyr	Leu	Leu	Trp	Leu	Leu	Leu	210	215	220	
Val	Thr	Leu	Ala	Tyr	Asn	Trp	Asn	Cys	Trp	Phe	Ile	Pro	Leu	Arg	Leu	225	230	235	
Val	Phe	Pro	Tyr	Gln	Thr	Ala	Asp	Asn	Ile	His	Tyr	Trp	Leu	Ile	Ala	245	250	255	
Asp	Ile	Ile	Cys	Asp	Ile	Ile	Tyr	Leu	Tyr	Asp	Met	Leu	Phe	Ile	Gln	260	265	270	



Pro	Arg	Leu	Gln	Phe	Val	Arg	Gly	Gly	Asp	Ile	Ile	Val	Asp	Ser	Asn	275	280	285
Glu	Leu	Arg	Lys	His	Tyr	Arg	Thr	Ser	Pro	Lys	Phe	Gln	Leu	Asp	Val	290	295	300
Ala	Ser	Ile	Ile	Pro	Phe	Asp	Ile	Cys	Tyr	Leu	Phe	Phe	Gly	Phe	Asn	305	310	315
Pro	Met	Phe	Arg	Ala	Asn	Arg	Met	Leu	Lys	Tyr	Thr	Ser	Phe	Phe	Glu	325	330	335
Phe	Asn	His	His	Leu	Glu	Ser	Ile	Met	Asp	Lys	Ala	Tyr	Ile	Tyr	Arg	340	345	350
Val	Ile	Arg	Thr	Thr	Gly	Tyr	Leu	Leu	Phe	Ile	Leu	His	Ile	Asn	Ala	355	360	365
Cys	Val	Tyr	Tyr	Trp	Ala	Ser	Asn	Tyr	Glu	Gly	Ile	Gly	Thr	Thr	Arg	370	375	380
Trp	Val	Tyr	Asp	Gly	Glu	Gly	Asn	Glu	Tyr	Leu	Arg	Cys	Tyr	Tyr	Trp	385	390	395
Ala	Val	Arg	Thr	Leu	Ile	Thr	Ile	Gly	Gly	Leu	Pro	Glu	Pro	Gln	Thr	405	410	415
Leu	Phe	Glu	Ile	Val	Phe	Gln	Leu	Leu	Asn	Phe	Phe	Ser	Gly	Val	Phe	420	425	430
Val	Phe	Ser	Ser	Leu	Ile	Gly	Gln	Met	Arg	Asp	Val	Ile	Gly	Ala	Ala	435	440	445
Thr	Ala	Asn	Gln	Asn	Tyr	Phe	Arg	Ala	Cys	Met	Asp	Asp	Thr	Ile	Ala	450	455	460
Tyr	Met	Asn	Asn	Tyr	Ser	Ile	Pro	Lys	Leu	Val	Gln	Lys	Arg	Val	Arg	465	470	475
Thr	Trp	Tyr	Glu	Tyr	Thr	Trp	Asp	Ser	Gln	Arg	Met	Leu	Asp	Glu	Ser	485	490	495
Asp	Leu	Leu	Lys	Thr	Leu	Pro	Thr	Thr	Val	Gln	Leu	Ala	Leu	Ala	Ile	500	505	510
Asp	Val	Asn	Phe	Ser	Ile	Ile	Ser	Lys	Val	Asp	Leu	Phe	Lys	Gly	Cys	515	520	525
Asp	Thr	Gln	Met	Ile	Tyr	Asp	Met	Leu	Leu	Arg	Leu	Lys	Ser	Val	Leu	530	535	540
Tyr	Leu	Pro	Gly	Asp	Phe	Val	Cys	Lys	Lys	Gly	Glu	Ile	Gly	Lys	Glu	545	550	555
Met	Tyr	Ile	Ile	Lys	His	Gly	Glu	Val	Gln	Val	Leu	Gly	Gly	Pro	Asp	565	570	575
Gly	Thr	Lys	Val	Leu	Val	Thr	Leu	Lys	Ala	Gly	Ser	Val	Phe	Gly	Glu	580	585	590

Ile Ser Leu Leu Ala Ala Gly Gly Gly Asn Arg Arg Thr Ala Asn Val  
 595 600 605  
 Val Ala His Gly Phe Ala Asn Leu Leu Thr Leu Asp Lys Lys Thr Leu  
 610 615 620  
 Gln Glu Ile Leu Val His Tyr Pro Asp Ser Glu Arg Ile Leu Met Lys  
 625 630 635 640  
 Lys Ala Arg Val Leu Leu Lys Gln Lys Ala Lys Thr Ala Glu Ala Thr  
 645 650 655  
 Pro Pro Arg Lys Asp Leu Ala Leu Leu Phe Pro Pro Lys Glu Glu Thr  
 660 665 670  
 Pro Lys Leu Phe Lys Thr Leu Leu Gly Gly Thr Gly Lys Ala Ser Leu  
 675 680 685  
 Ala Arg Leu Leu Lys Leu Lys Arg Glu Gln Ala Ala Gln Lys Lys Glu  
 690 695 700  
 Asn Ser Glu Gly Gly Glu Glu Glu Gly Lys Glu Asn Glu Asp Lys Gln  
 705 710 715 720  
 Lys Glu Asn Glu Asp Lys Gln Lys Glu Asn Glu Asp Lys Gly Lys Glu  
 725 730 735  
 Asn Glu Asp Lys Asp Lys Gly Arg Glu Pro Glu Glu Lys Pro Leu Asp  
 740 745 750  
 Arg Pro Glu Cys Thr Ala Ser Pro Ile Ala Val Glu Glu Glu Pro His  
 755 760 765  
 Ser Val Arg Arg Thr Val Leu Pro Arg Gly Thr Ser Arg Gln Ser Leu  
 770 775 780  
 Ile Ile Ser Met Ala Pro Ser Ala Glu Gly Gly Glu Glu Val Leu Thr  
 785 790 795 800  
 Ile Glu Val Lys Glu Lys Ala Lys Gln  
 805

<210> 14  
 <211> 694  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CNGA1

<400> 14  
 Met Ala Lys Ile Asn Thr Gln Tyr Ser His Pro Ser Arg Thr His Leu  
 1 5 10 15  
 Lys Val Lys Thr Ser Asp Arg Asp Leu Asn Arg Ala Glu Asn Gly Leu  
 20 25 30  
 Ser Arg Ala His Ser Ser Ser Glu Glu Thr Ser Ser Val Leu Gln Pro  
 35 40 45

Gly	Ile	Ala	Met	Glu	Thr	Arg	Gly	Leu	Ala	Asp	Ser	Gly	Gln	Gly	Ser	50	55	60	
Phe	Thr	Gly	Gln	Gly	Ile	Ala	Arg	Leu	Ser	Arg	Leu	Ile	Phe	Leu	Leu	65	70	75	80
Arg	Arg	Trp	Ala	Ala	Arg	His	Val	His	His	Gln	Asp	Gln	Gly	Pro	Asp	85	90	95	
Ser	Phe	Pro	Asp	Arg	Phe	Arg	Gly	Ala	Glu	Leu	Lys	Glu	Val	Ser	Ser	100	105	110	
Gln	Glu	Ser	Asn	Ala	Gln	Ala	Asn	Val	Gly	Ser	Gln	Glu	Pro	Ala	Asp	115	120	125	
Arg	Gly	Arg	Ser	Ala	Trp	Pro	Leu	Ala	Lys	Cys	Asn	Thr	Asn	Thr	Ser	130	135	140	
Asn	Asn	Thr	Glu	Glu	Glu	Lys	Lys	Thr	Lys	Lys	Lys	Asp	Ala	Ile	Val	145	150	155	160
Val	Asp	Pro	Ser	Ser	Asn	Leu	Tyr	Tyr	Arg	Trp	Leu	Thr	Ala	Ile	Ala	165	170	175	
Leu	Pro	Val	Phe	Tyr	Asn	Trp	Tyr	Leu	Leu	Ile	Cys	Arg	Ala	Cys	Phe	180	185	190	
Asp	Glu	Leu	Gln	Ser	Glu	Tyr	Leu	Met	Leu	Trp	Leu	Val	Leu	Asp	Tyr	195	200	205	
Ser	Ala	Asp	Val	Leu	Tyr	Val	Leu	Asp	Val	Leu	Val	Arg	Ala	Arg	Thr	210	215	220	
Gly	Phe	Leu	Glu	Gln	Gly	Leu	Met	Val	Ser	Asp	Thr	Asn	Arg	Leu	Trp	225	230	235	240
Gln	His	Tyr	Lys	Thr	Thr	Thr	Gln	Phe	Lys	Leu	Asp	Val	Leu	Ser	Leu	245	250	255	
Val	Pro	Thr	Asp	Leu	Ala	Tyr	Leu	Lys	Val	Gly	Thr	Asn	Tyr	Pro	Glu	260	265	270	
Val	Arg	Phe	Asn	Arg	Leu	Leu	Lys	Phe	Ser	Arg	Leu	Phe	Glu	Phe	Phe	275	280	285	
Asp	Arg	Thr	Glu	Thr	Arg	Thr	Asn	Tyr	Pro	Asn	Met	Phe	Arg	Ile	Gly	290	295	300	
Asn	Leu	Val	Leu	Tyr	Ile	Leu	Ile	Ile	Ile	His	Trp	Asn	Ala	Cys	Ile	305	310	315	320
Tyr	Phe	Ala	Ile	Ser	Lys	Phe	Ile	Gly	Phe	Gly	Thr	Asp	Ser	Trp	Val	325	330	335	
Tyr	Pro	Asn	Ile	Ser	Ile	Pro	Glu	His	Gly	Arg	Leu	Ser	Arg	Lys	Tyr	340	345	350	
Ile	Tyr	Ser	Leu	Tyr	Trp	Ser	Thr	Leu	Thr	Leu	Thr	Thr	Ile	Gly	Glu	355	360	365	

Thr	Pro	Pro	Pro	Val	Lys	Asp	Glu	Glu	Tyr	Leu	Phe	Val	Val	Val	Asp
370						375					380				
Phe	Leu	Val	Gly	Val	Leu	Ile	Phe	Ala	Thr	Ile	Val	Gly	Asn	Val	Gly
385					390					395					400
Ser	Met	Ile	Ser	Asn	Met	Asn	Ala	Ser	Arg	Ala	Glu	Phe	Gln	Ala	Lys
				405					410					415	
Ile	Asp	Ser	Ile	Lys	Gln	Tyr	Met	Gln	Phe	Arg	Lys	Val	Thr	Lys	Asp
			420					425					430		
Leu	Glu	Thr	Arg	Val	Ile	Arg	Trp	Phe	Asp	Tyr	Leu	Trp	Ala	Asn	Lys
		435					440					445			
Lys	Thr	Val	Asp	Glu	Lys	Glu	Val	Leu	Lys	Ser	Leu	Pro	Asp	Lys	Leu
	450					455					460				
Lys	Ala	Glu	Ile	Ala	Ile	Asn	Val	His	Leu	Asp	Thr	Leu	Lys	Lys	Val
465					470					475					480
Arg	Ile	Phe	Gln	Asp	Cys	Glu	Ala	Gly	Leu	Leu	Val	Glu	Leu	Val	Leu
				485					490						495
Lys	Leu	Arg	Pro	Thr	Val	Phe	Ser	Pro	Gly	Asp	Tyr	Ile	Cys	Lys	Lys
			500					505					510		
Gly	Asp	Ile	Gly	Lys	Glu	Met	Tyr	Ile	Ile	Asn	Glu	Gly	Lys	Leu	Ala
		515					520					525			
Val	Val	Ala	Asp	Asp	Gly	Val	Thr	Gln	Phe	Val	Val	Leu	Ser	Asp	Gly
	530					535					540				
Ser	Tyr	Phe	Gly	Glu	Ile	Ser	Ile	Leu	Asn	Ile	Lys	Gly	Ser	Lys	Ser
545					550					555					560
Gly	Asn	Arg	Arg	Thr	Ala	Asn	Ile	Arg	Ser	Ile	Gly	Tyr	Ser	Asp	Leu
				565					570					575	
Phe	Cys	Leu	Ser	Lys	Asp	Asp	Leu	Met	Glu	Ala	Leu	Thr	Glu	Tyr	Pro
			580					585					590		
Glu	Ala	Lys	Lys	Ala	Leu	Glu	Glu	Lys	Gly	Arg	Gln	Ile	Leu	Met	Lys
		595						600				605			
Asp	Asn	Leu	Ile	Asp	Glu	Glu	Leu	Ala	Arg	Ala	Gly	Ala	Asp	Pro	Lys
	610					615					620				
Asp	Leu	Glu	Glu	Lys	Val	Glu	Gln	Leu	Gly	Ser	Ser	Leu	Asp	Thr	Leu
625					630					635					640
Gln	Thr	Arg	Phe	Ala	Arg	Leu	Leu	Ala	Glu	Tyr	Asn	Ala	Thr	Gln	Met
				645					650					655	
Lys	Met	Lys	Gln	Arg	Leu	Ser	Gln	Leu	Glu	Ser	Gln	Val	Lys	Gly	Gly
			660					665					670		

Gly Asp Lys Pro Leu Ala Asp Gly Glu Val Pro Gly Asp Ala Thr Lys  
 675 680 685

Thr Glu Asp Lys Gln Gln  
 690

<210> 15

<211> 690

<212> PRT

<213> Homo sapiens

<220>

<223> CNGA3

<400> 15

Met Lys Leu Ser Met Lys Asn Asn Ile Ile Asn Thr Gln Gln Ser Phe  
 1 5 10 15

Val Thr Met Pro Asn Val Ile Val Pro Asp Ile Glu Lys Glu Ile Arg  
 20 25 30

Arg Met Glu Asn Gly Ala Cys Ser Ser Phe Ser Glu Asp Asp Asp Ser  
 35 40 45

Ala Ser Thr Ser Glu Glu Ser Glu Asn Glu Asn Pro His Ala Arg Gly  
 50 55 60

Ser Phe Ser Tyr Lys Ser Leu Arg Lys Gly Gly Pro Ser Gln Arg Glu  
 65 70 75 80

Gln Tyr Leu Pro Gly Ala Ile Ala Leu Phe Asn Val Asn Asn Ser Ser  
 85 90 95

Asn Lys Asp Gln Glu Pro Glu Glu Lys Lys Lys Lys Lys Lys Glu Lys  
 100 105 110

Lys Ser Lys Ser Asp Asp Lys Asn Glu Asn Lys Asn Asp Pro Glu Lys  
 115 120 125

Lys Lys Lys Lys Lys Asp Lys Glu Lys Lys Lys Lys Glu Glu Lys Ser  
 130 135 140

Lys Asp Lys Lys Glu Glu Glu Lys Lys Glu Val Val Val Ile Asp Pro  
 145 150 155 160

Ser Gly Asn Thr Tyr Tyr Asn Trp Leu Phe Cys Ile Thr Leu Pro Val  
 165 170 175

Met Tyr Asn Trp Thr Met Val Ile Ala Arg Ala Cys Phe Asp Glu Leu  
 180 185 190

Gln Ser Asp Tyr Leu Glu Tyr Trp Leu Ile Leu Asp Tyr Val Ser Asp  
 195 200 205

Ile Val Tyr Leu Ile Asp Met Phe Val Arg Thr Arg Thr Gly Tyr Leu  
 210 215 220

Glu Gln Gly Leu Leu Val Lys Glu Glu Leu Lys Leu Ile Asn Lys Tyr  
 225 230 235 240

Lys	Ser	Asn	Leu	Gln	Phe	Lys	Leu	Asp	Val	Leu	Ser	Leu	Ile	Pro	Thr	
				245					250					255		
Asp	Leu	Leu	Tyr	Phe	Lys	Leu	Gly	Trp	Asn	Tyr	Pro	Glu	Ile	Arg	Leu	
			260					265					270			
Asn	Arg	Leu	Leu	Arg	Phe	Ser	Arg	Met	Phe	Glu	Phe	Phe	Gln	Arg	Thr	
		275					280					285				
Glu	Thr	Arg	Thr	Asn	Tyr	Pro	Asn	Ile	Phe	Arg	Ile	Ser	Asn	Leu	Val	
	290					295					300					
Met	Tyr	Ile	Val	Ile	Ile	Ile	His	Trp	Asn	Ala	Cys	Val	Phe	Tyr	Ser	
305					310					315					320	
Ile	Ser	Lys	Ala	Ile	Gly	Phe	Gly	Asn	Asp	Thr	Trp	Val	Tyr	Pro	Asp	
			325					330						335		
Ile	Asn	Asp	Pro	Glu	Phe	Gly	Arg	Leu	Ala	Arg	Lys	Tyr	Val	Tyr	Ser	
			340					345					350			
Leu	Tyr	Trp	Ser	Thr	Leu	Thr	Leu	Thr	Thr	Ile	Gly	Glu	Thr	Pro	Pro	
		355					360					365				
Pro	Val	Arg	Asp	Ser	Glu	Tyr	Val	Phe	Val	Val	Val	Asp	Phe	Leu	Ile	
	370					375					380					
Gly	Val	Leu	Ile	Phe	Ala	Thr	Ile	Val	Gly	Asn	Ile	Gly	Ser	Met	Ile	
385					390					395					400	
Ser	Asn	Met	Asn	Ala	Ala	Arg	Ala	Glu	Phe	Gln	Ala	Arg	Ile	Asp	Ala	
				405					410					415		
Ile	Lys	Gln	Tyr	Met	His	Phe	Arg	Asn	Val	Ser	Lys	Asp	Met	Glu	Lys	
		420						425					430			
Arg	Val	Ile	Lys	Trp	Phe	Asp	Tyr	Leu	Trp	Thr	Asn	Lys	Lys	Thr	Val	
		435					440					445				
Asp	Glu	Lys	Glu	Val	Leu	Lys	Tyr	Leu	Pro	Asp	Lys	Leu	Arg	Ala	Glu	
	450					455					460					
Ile	Ala	Ile	Asn	Val	His	Leu	Asp	Thr	Leu	Lys	Lys	Val	Arg	Ile	Phe	
465					470					475					480	
Ala	Asp	Cys	Glu	Ala	Gly	Leu	Leu	Val	Glu	Leu	Val	Leu	Lys	Leu	Gln	
				485					490					495		
Pro	Gln	Val	Tyr	Ser	Pro	Gly	Asp	Tyr	Ile	Cys	Lys	Lys	Gly	Asp	Ile	
		500						505					510			
Gly	Arg	Glu	Met	Tyr	Ile	Ile	Lys	Glu	Gly	Lys	Leu	Ala	Val	Val	Ala	
		515					520					525				
Asp	Asp	Gly	Val	Thr	Gln	Phe	Val	Val	Leu	Ser	Asp	Gly	Ser	Tyr	Phe	
	530					535					540					
Gly	Glu	Ile	Ser	Ile	Leu	Asn	Ile	Lys	Gly	Ser	Lys	Ala	Gly	Asn	Arg	
545					550					555					560	

Arg Thr Ala Asn Ile Lys Ser Ile Gly Tyr Ser Asp Leu Phe Cys Leu  
                   565                                  570                                  575  
 Ser Lys Asp Asp Leu Met Glu Ala Leu Thr Glu Tyr Pro Asp Ala Lys  
                   580                                  585                                  590  
 Thr Met Leu Glu Glu Lys Gly Lys Gln Ile Leu Met Lys Asp Gly Leu  
                   595                                  600                                  605  
 Leu Asp Leu Asn Ile Ala Asn Ala Gly Ser Asp Pro Lys Asp Leu Glu  
                   610                                  615                                  620  
 Glu Lys Val Thr Arg Met Glu Gly Ser Val Asp Leu Leu Gln Thr Arg  
                   625                                  630                                  635                                  640  
 Phe Ala Arg Ile Leu Ala Glu Tyr Glu Ser Met Gln Gln Lys Leu Lys  
                   645                                  650                                  655  
 Gln Arg Leu Thr Lys Val Glu Lys Phe Leu Lys Pro Leu Ile Asp Thr  
                   660                                  665                                  670  
 Glu Phe Ser Ser Ile Glu Gly Pro Gly Ala Glu Ser Gly Pro Ile Asp  
                   675                                  680                                  685  
 Ser Thr  
                   690

<210> 16

<211> 2757

<212> DNA

<213> Homo sapiens

<220>

<223> complete CNG3B sequence derived from assembly of  
 PCR fragments

<220>

<221> CDS

<222> (112) .. (2541)

<223> CNG3B

<400> 16

```

ccatcctaatac gactcact atagggctcg agcggccgcc cgggcaggtc atttctctac 60
cttaaggcac agtcataaat acagagggtt ttcagaacca cctcagagaa gatgttttaa 120
tcgctgacaa aagtcaacaa ggtgaagcct ataggagaga acaatgagaa tgaacaaagt 180
tctcgtcgga atgaagaagg ctctcaccac agtaatcagt ctcagcaaac cacagcacag 240
gaagaaaaca aaggtgaaga gaaatctctc aaaaccaagt caactccagt cacgtctgaa 300
gagccacaca ccaacataca agacaaactc tccaagaaaa attcctctgg agatctgacc 360
acaaaccctg accctcaaaa tgcagcagaa ccaactggaa cagtgccaga gcagaaggaa 420
atggaccccg ggaaagaagg tccaaacagc ccacaaaaca aaccgcctgc agctcctggt 480
ataaatgagt atgccgatgc ccagctacac aacctgggtg aaagaatgcg tcaaagaaca 540
gccctctaca agaaaaagtt ggtagagggg gatctctcct caccgaagc cagcccacaa 600
actgcaaagc ccacggctgt accaccagta aaagaaagcg atgataagcc aacagaacat 660
tactacaggc tgttgtggtt caaagtcaaa aagatgcctt taacagagta cttaaagcga 720
attaaacttc caaacagcat agattcatac acagatcgac tctatctcct gtggctcttg 780
cttgctactc ttgcctataa ctggaactgc tggtttatac cactgcccct cgtcttccca 840
tatcaaaccg cagacaacat acactactgg cttattgcgg acatcatatg tgatatcatc 900
tacctttatg atatgctatt tatccagccc agactccagt ttgtaagagg aggagacata 960
atagtggatt caaatgagct aaggaaacac tacaggactt ctacaaaatt tcagttggat 1020
gtcgcaccaa taataccatt tgatatattgc tacctcttct ttgggtttta tccaatgttt 1080

```

agagcaaata	ggatgttaaa	gtacacttca	ttttttgaat	ttaatcatca	cctagagtct	1140
ataatggaca	aagcatatat	ctacagagtt	attcgaacaa	ctggatactt	gctgttttatt	1200
ctgcacatta	atgcctgtgt	ttattactgg	gcttcaaact	atgaaggaat	tggcactact	1260
agatgggtgt	atgatgggga	aggaaacgag	tatctgagat	gttattattg	ggcagttcga	1320
actttaatta	ccattggtgg	ccttccagaa	ccacaaactt	tatttgaaat	tgtttttcaa	1380
ctcttgaatt	ttttttctgg	agtttttgtg	ttctccagtt	taattggtca	gatgagagat	1440
gtgattggag	cagctacagc	caatcagaac	tacttccgcg	cctgcatgga	tgacaccatt	1500
gcctacatga	acaattactc	cattcctaaa	cttgtgcaaa	agcgagtctg	gacttggtat	1560
gaatatacat	gggactctca	aagaatgcta	gatgagtctg	at ttgcttaa	gaccctacca	1620
actacgggtcc	agttagccct	cgccattgat	gtgaacttca	gcatcatcag	caaagtcgac	1680
ttgttcaagg	gttgtgatac	acagatgatt	tatgacatgt	tgctaagatt	gaaatccgtt	1740
ctctattttgc	ctggtgactt	tgtctgcaaa	aaggagaaaa	ttggcaagga	aatgtatatc	1800
atcaagcatg	gagaagtcca	agttcttgga	ggcctgatg	gtactaaagt	tctgggttact	1860
ctgaaagctg	ggtcggtgtt	tggagaaatc	agccttctag	cagcaggagg	aggaaaccgt	1920
cgaactgcc	atgtggtggc	ccacgggttt	gccaatcttt	taactctaga	caaaaagacc	1980
ctccaagaaa	ttctagtgc	ttatccagat	tctgaaagga	tcctcatgaa	gaaagccaga	2040
gtgcttttaa	agcagaaggc	taagaccgca	gaagcaaccc	ctccaagaaa	agatcttgcc	2100
ctcctcttcc	caccgaaaga	agagacaccc	aaactgttta	aaactctcct	aggaggcaca	2160
ggaaaagcaa	gtcttgcaag	actactcaaa	ttgaagcgag	agcaagcagc	tcagaagaaa	2220
gaaaattctg	aaggaggaga	ggaagaagga	aaagaaaatg	aagataaaca	aaaagaaaat	2280
gaagataaac	aaaaagaaaa	tgaagataaa	ggaaaagaaa	atgaagataa	agataaagga	2340
agagagccag	aagagaagcc	actggacaga	cctgaatgta	cagcaagtcc	tattgcagtg	2400
gaggaagaac	cccactcagt	tagaaggaca	gttttacc	gagggacttc	tcgtcaatca	2460
ctcattatca	gcatggctcc	ttctgctgag	ggcggagaag	aggttcttac	tattgaagtc	2520
aaagaaaagg	ctaagcaata	aatgtttgat	tatctttaga	tgtgatatag	ctagttccca	2580
aagtgattgt	acctaggatt	gtaacttaaa	ttaacgaggg	gaaacgacat	gctgggaccc	2640
ttgagaaacg	aaaggcaaat	ccctagctta	gtttctagga	cttatctgag	agtgtgattt	2700
catgcagtgg	taataagaag	attattaaaa	gcaaaaaaaaa	aaaaaaaaaa	aaaaaaa	2757